



PCT

## RAW SEQUENCE LISTING

DATE: 02/22/2005

PATENT APPLICATION: US/10/522,427

TIME: 13:32:22

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\02222005\J522427.raw

3 <110> APPLICANT: Commonwealth Scientific and Industrial Research Organisation  
W--> 4 <120> TITLE OF INVENTION: Expression system  
W--> 5 <130> FILE REFERENCE: 13447210  
C--> 6 <140> CURRENT APPLICATION NUMBER: US/10/522,427  
C--> 6 <141> CURRENT FILING DATE: 2005-01-25  
W--> 6 <160> NUMBER OF SEQ ID: 40  
7 <170> SOFTWARE: PatentIn version 3.2

## ERRORED SEQUENCES

561 <210> SEQ ID NO: 40  
562 <211> LENGTH: 30  
563 <212> TYPE: DNA  
564 <213> ORGANISM: Artificial Sequence  
W--> 565 <220> FEATURE:  
566 <223> OTHER INFORMATION: oligonucleotide  
W--> 567 <400> SEQUENCE: 40  
568 gtctaaaagc tttaccagt ttagctttag.  
E--> 573 19/22  
E--> 575 1/22

Does Not Comply  
Corrected Diskette Needed  
(pg. 1)

30

deleted

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L:4 M:283 W: Missing Blank Line separator, <120> field identifier  
L:5 M:283 W: Missing Blank Line separator, <130> field identifier  
L:6 M:270 C: Current Application Number differs, Replaced Current Application No  
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:6 M:283 W: Missing Blank Line separator, <160> field identifier  
L:13 M:283 W: Missing Blank Line separator, <220> field identifier  
L:15 M:283 W: Missing Blank Line separator, <400> field identifier  
L:25 M:283 W: Missing Blank Line separator, <220> field identifier  
L:27 M:283 W: Missing Blank Line separator, <400> field identifier  
L:40 M:283 W: Missing Blank Line separator, <220> field identifier  
L:42 M:283 W: Missing Blank Line separator, <400> field identifier  
L:54 M:283 W: Missing Blank Line separator, <220> field identifier  
L:56 M:283 W: Missing Blank Line separator, <400> field identifier  
L:66 M:283 W: Missing Blank Line separator, <220> field identifier  
L:68 M:283 W: Missing Blank Line separator, <400> field identifier  
L:78 M:283 W: Missing Blank Line separator, <220> field identifier  
L:80 M:283 W: Missing Blank Line separator, <400> field identifier  
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L:94 M:283 W: Missing Blank Line separator, <400> field identifier  
L:106 M:283 W: Missing Blank Line separator, <220> field identifier  
L:108 M:283 W: Missing Blank Line separator, <400> field identifier  
L:120 M:283 W: Missing Blank Line separator, <220> field identifier  
L:122 M:283 W: Missing Blank Line separator, <400> field identifier  
L:134 M:283 W: Missing Blank Line separator, <220> field identifier  
L:136 M:283 W: Missing Blank Line separator, <400> field identifier  
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L:254 M:283 W: Missing Blank Line separator, <400> field identifier  
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L:268 M:283 W: Missing Blank Line separator, <400> field identifier  
L:280 M:283 W: Missing Blank Line separator, <220> field identifier  
L:282 M:283 W: Missing Blank Line separator, <400> field identifier  
L:292 M:283 W: Missing Blank Line separator, <220> field identifier

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L:294 M:283 W: Missing Blank Line separator, <400> field identifier  
L:306 M:283 W: Missing Blank Line separator, <220> field identifier  
L:308 M:283 W: Missing Blank Line separator, <400> field identifier  
L:320 M:283 W: Missing Blank Line separator, <220> field identifier  
L:573 M:254 E: No. of Bases conflict, LENGTH:Input:22 Counted:31 SEQ:40  
L:573 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3  
M:254 Repeated in SeqNo=40  
L:575 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
L:575 M:252 E: No. of Seq. differs, <211> LENGTH:Input:30 Found:32 SEQ:40